



Signal Specificity in Practice and Theory

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EPA International Science Forum on Computational Toxicology

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Outline

- I. **Signal specificity in the yeast mating and starvation pathways**
- II. Kinetic insulation as mechanism for signal specificity

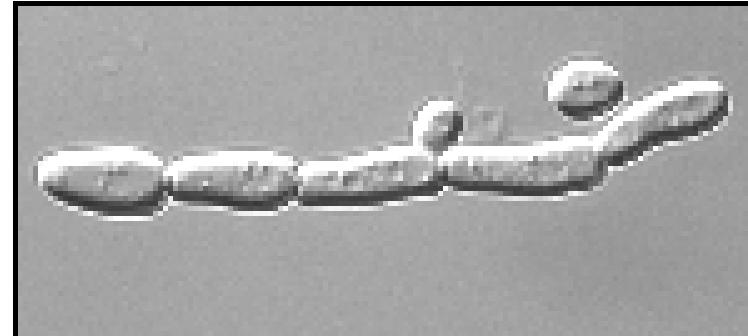
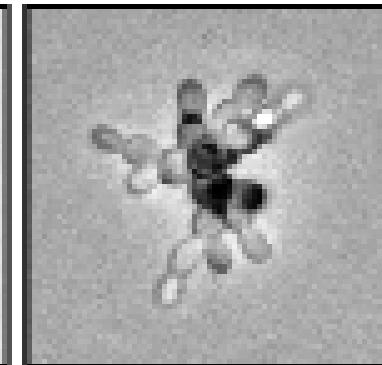
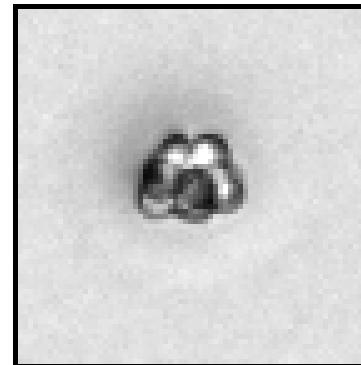


Two developmental behaviors

Mating differentiation

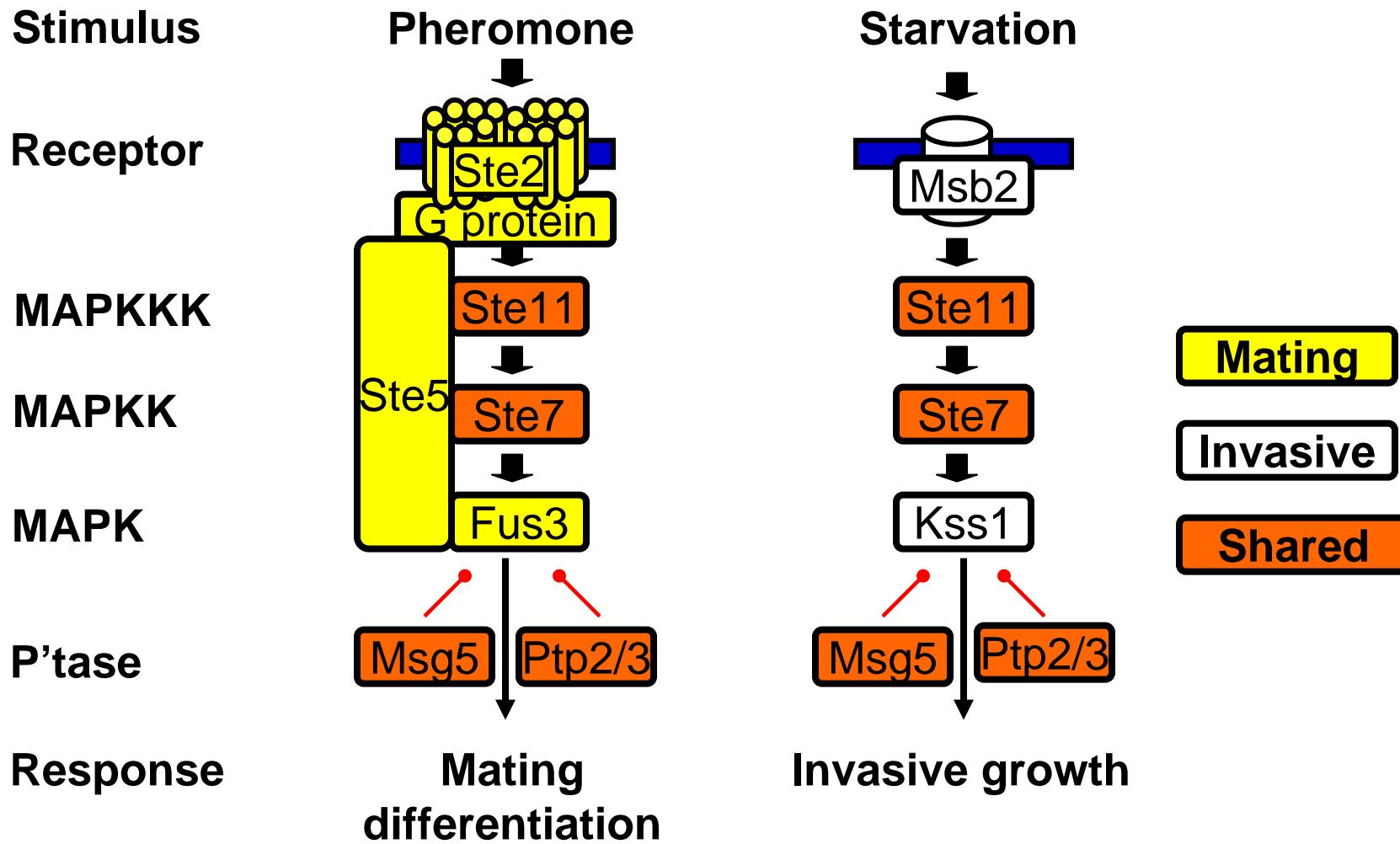


Invasive growth



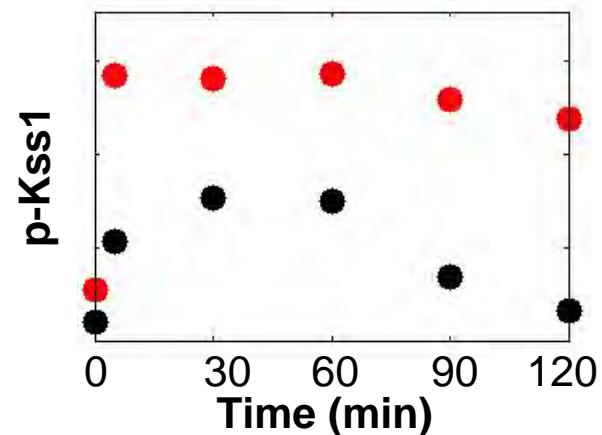
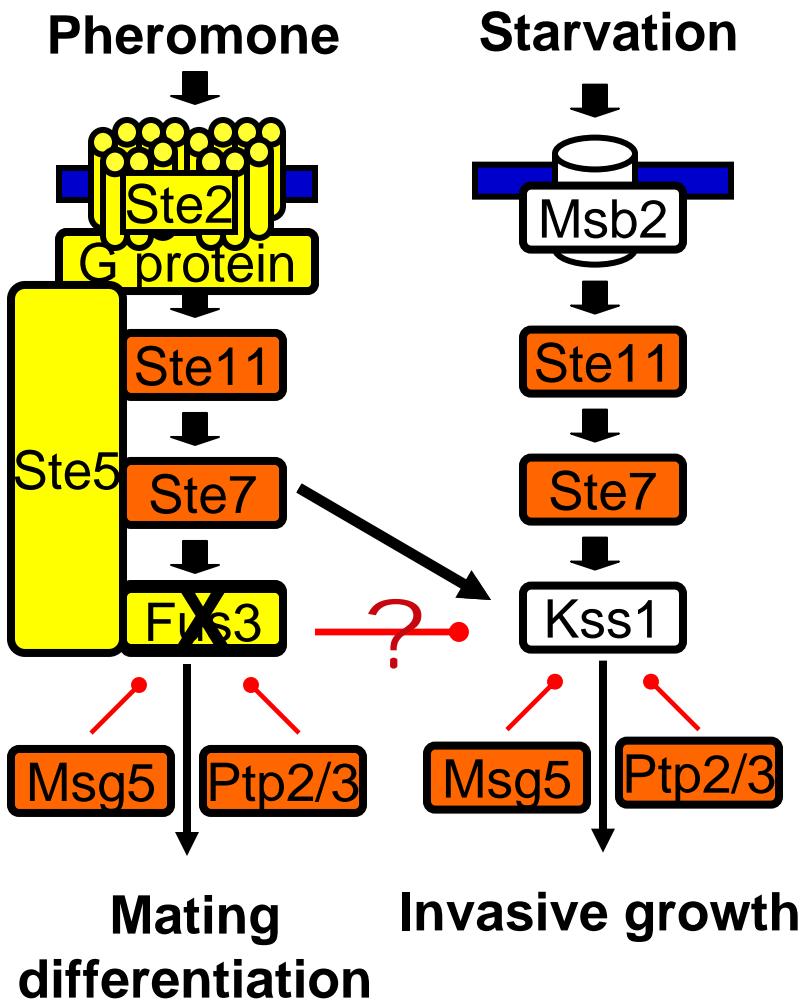


Signaling pathways with shared components





Fus3 diminishes activation of *Kss1*

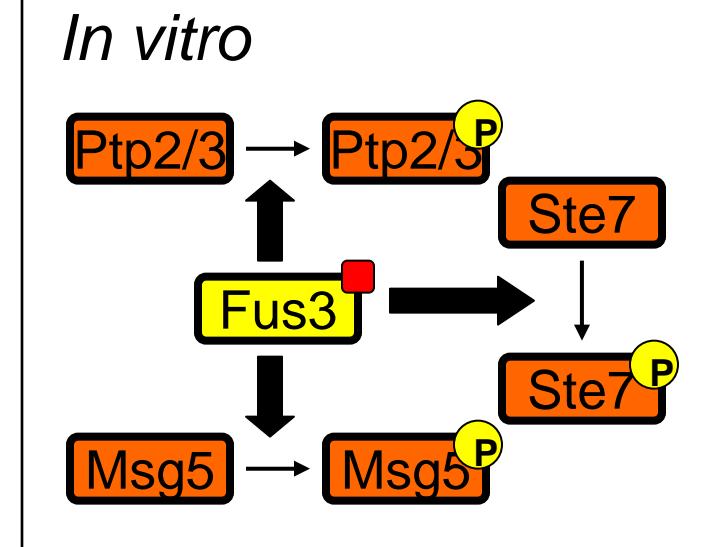
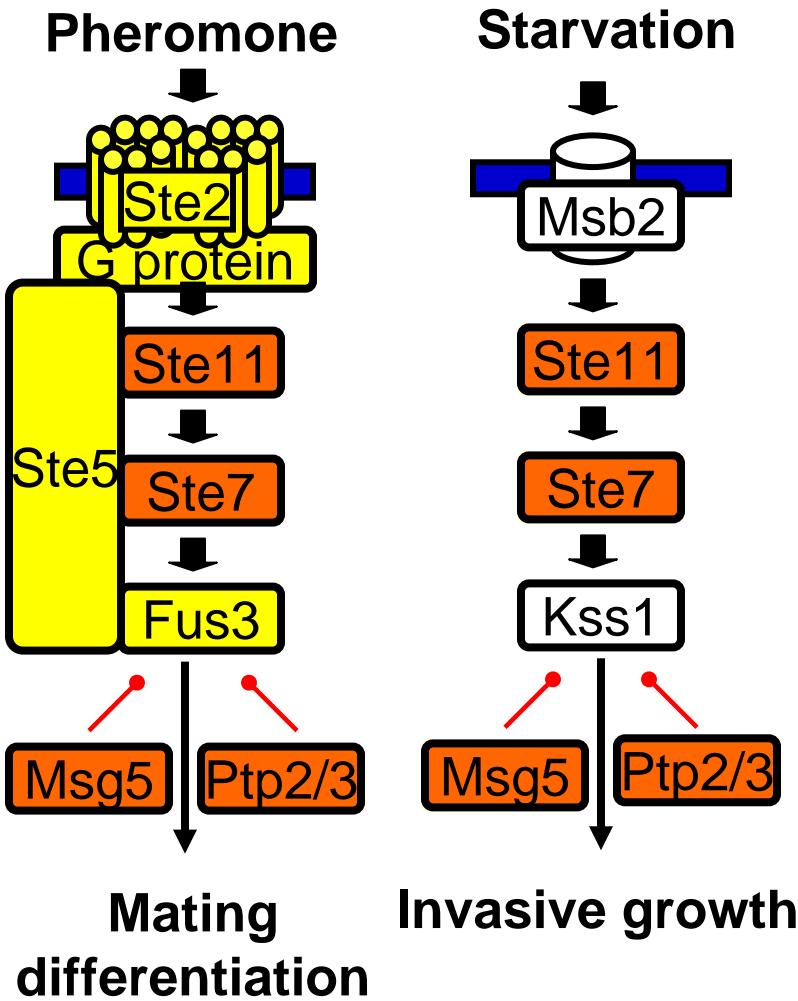


How does Fus3 diminish Kss1 activity?

W. Sabbagh, Jr., L. J. Flatauer, A. J. Bardwell, L. Bardwell, *Mol Cell* 8, 683 (2001)



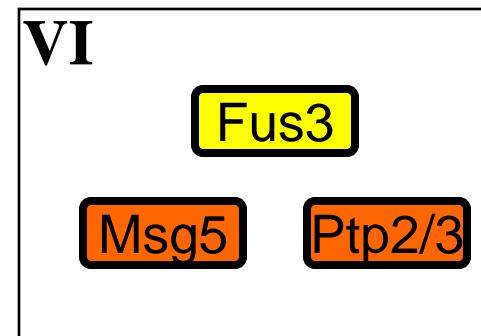
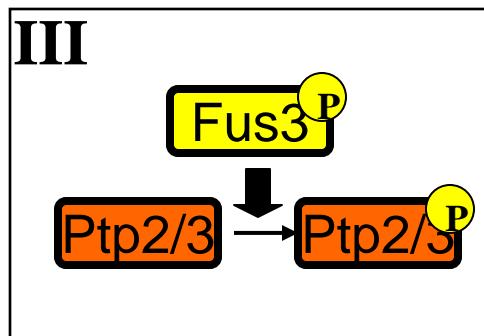
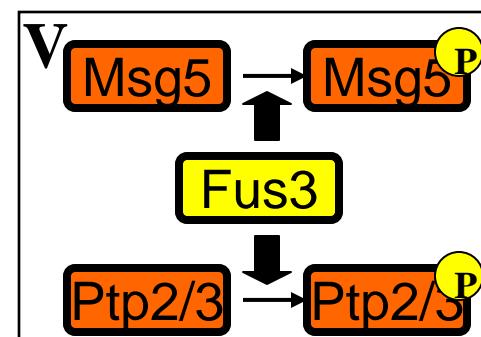
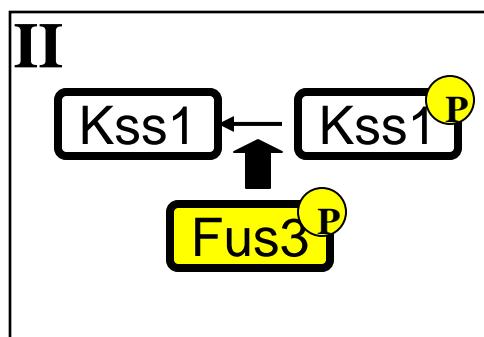
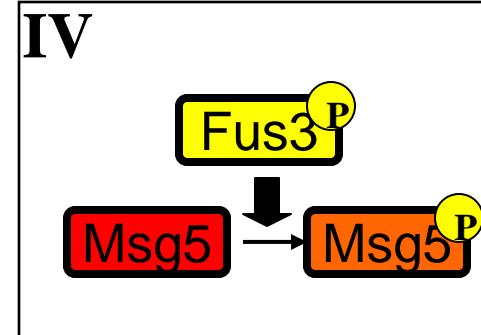
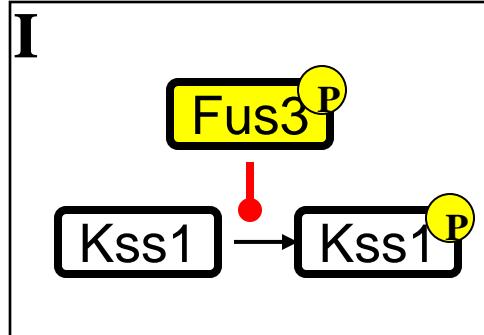
Fus3 phosphorylates shared components



Fus3 may diminish Kss1 activity by phosphorylating shared pathway components.



Six Models of Signal Specificity



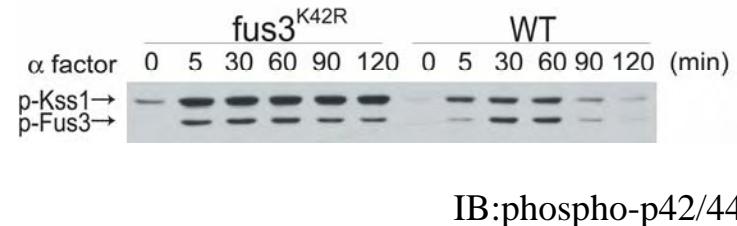


Research Design

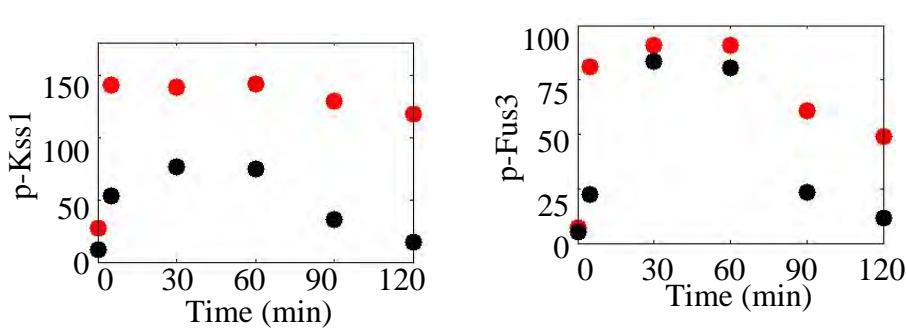
Model construction

$$\frac{d\mathbf{c}}{dt} = \mathbf{f}(\mathbf{c}, t)$$

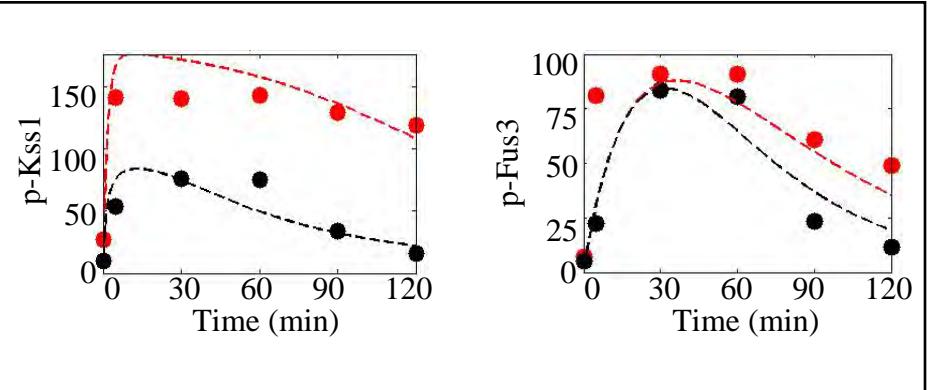
Time course of MAPK activation



Quantification by densitometry



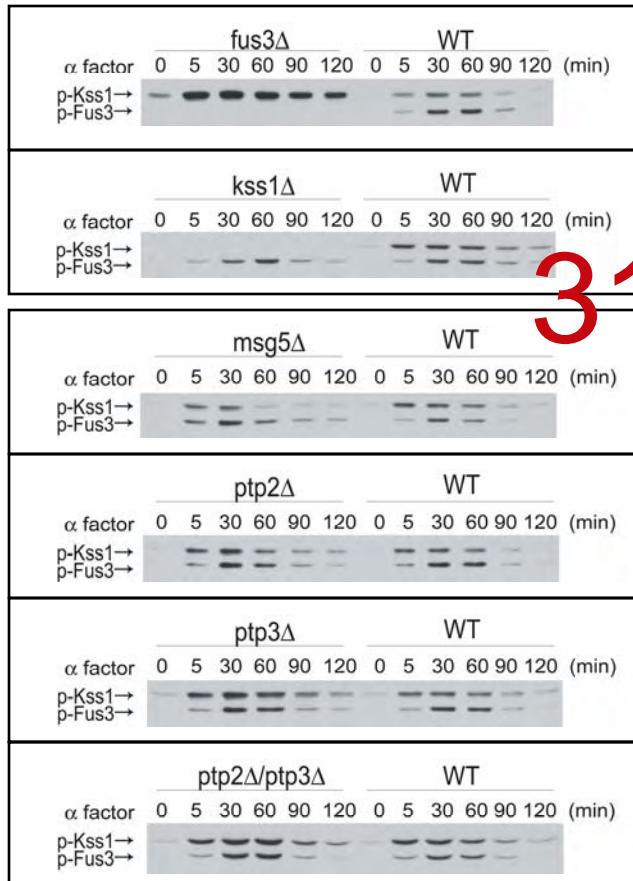
Fit models to the experimental results



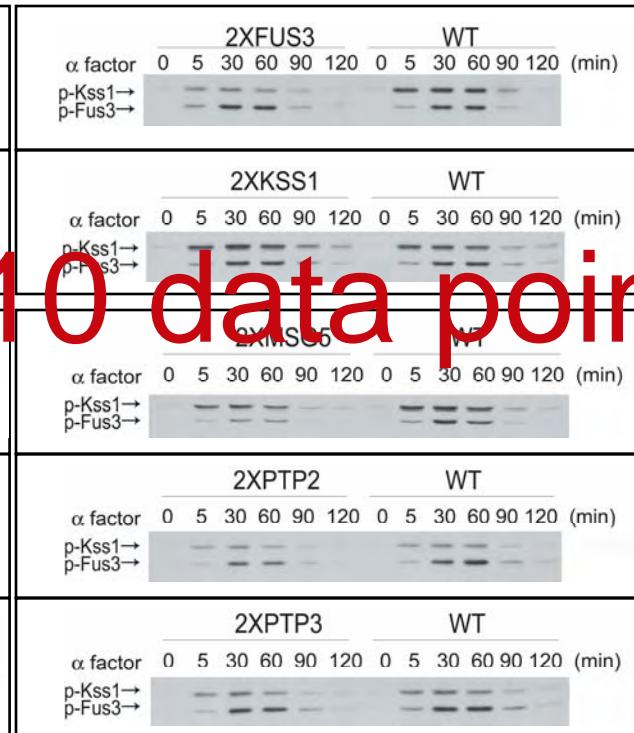


Experimental Results

Deletion



2-fold overexpression



Protein induction



310 data points

IB:phospho-p42/44

	Deletion	2-fold over expression
MAPK	fus3 Δ	2XFUS3
	kss1 Δ	2XKSS1
P' tase	msg5 Δ	2XMSG5
	ptp2 Δ	2XPTP2
	ptp3 Δ	2XPTP3
	ptp2/3 Δ	

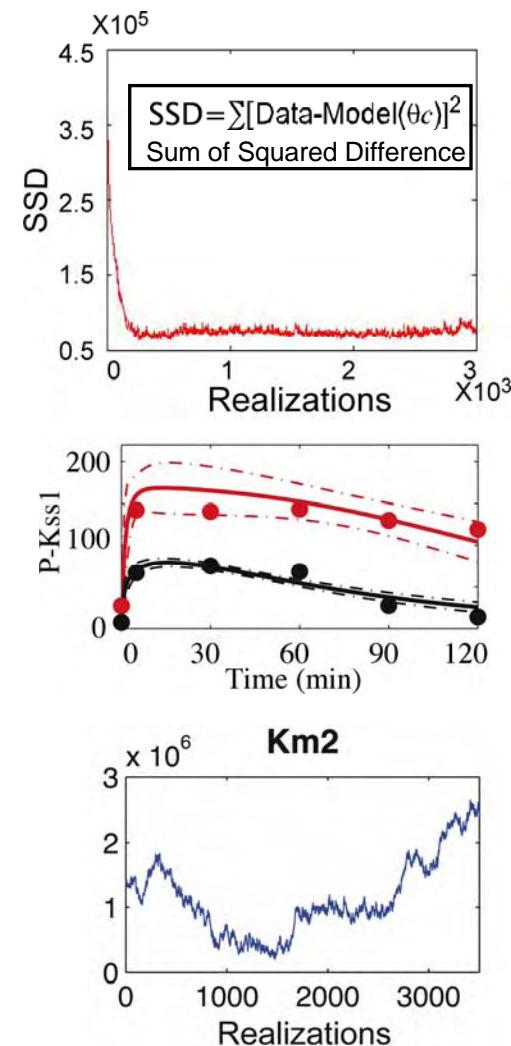
	Mutant
MAPK	fus3 ^{K42R}



Markov Chain Monte Carlo Methods (MCMC)

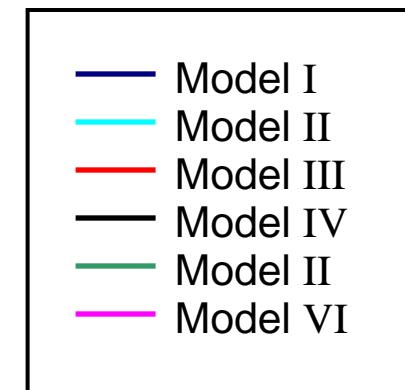
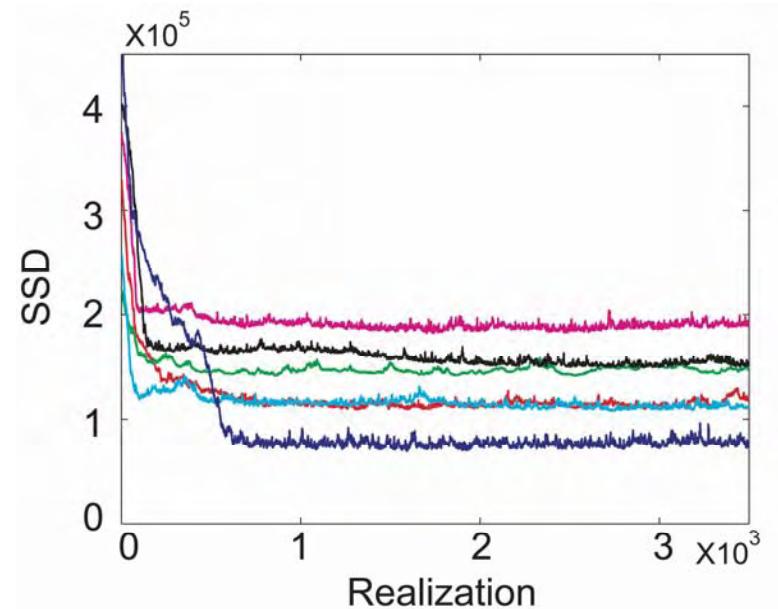
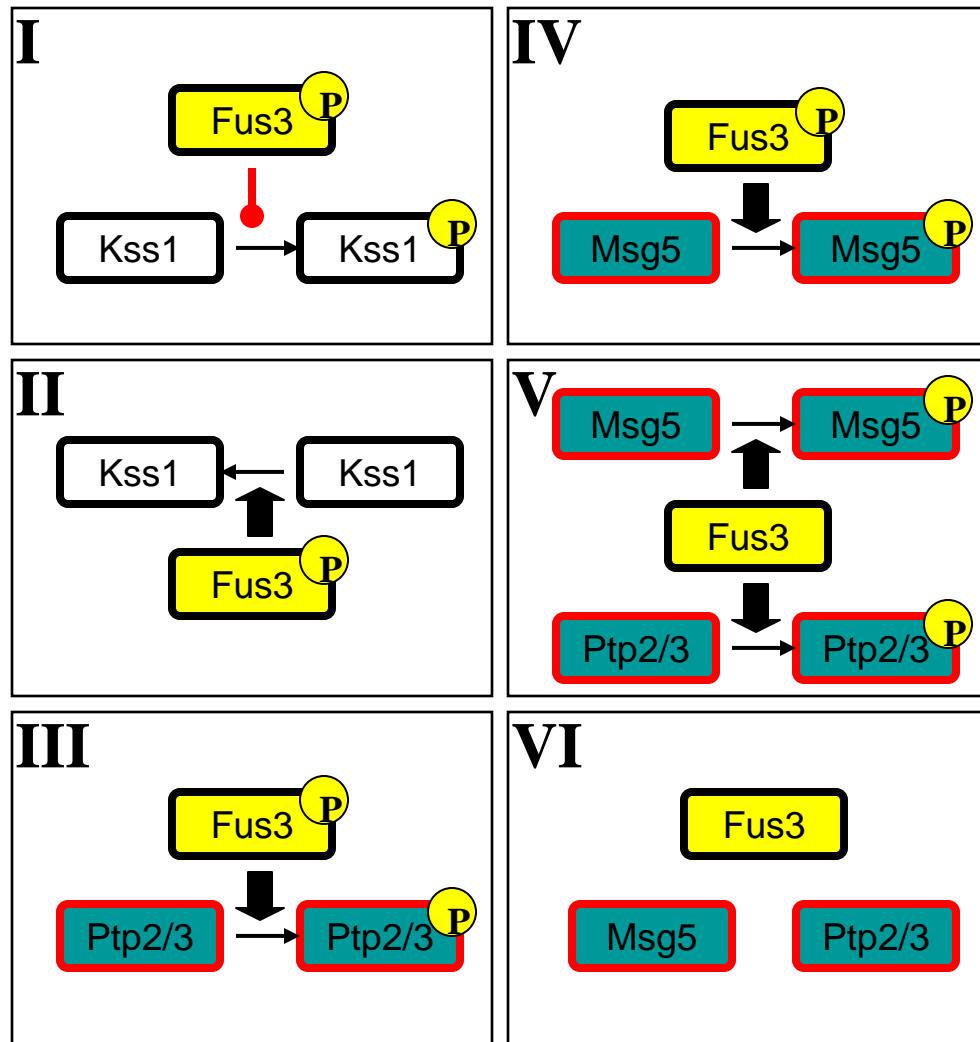
Advantages

- Method generates a family of parameter sets that each produces approximately equivalent fits to the data
- Method allows confidence intervals to be placed on model outputs
- Method generates a distribution of model parameters that provides a measure of how well the experimental data constrain the model.



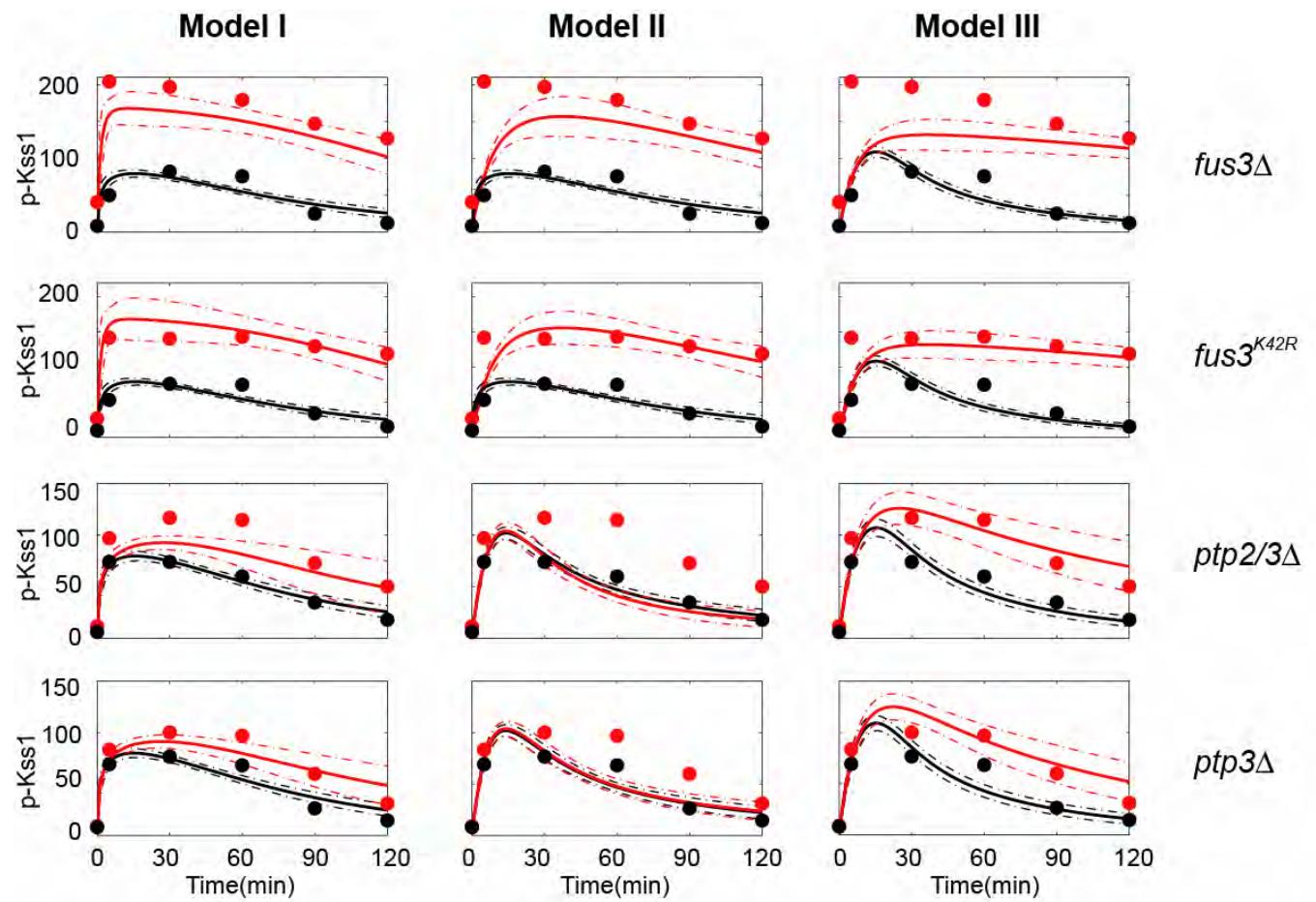
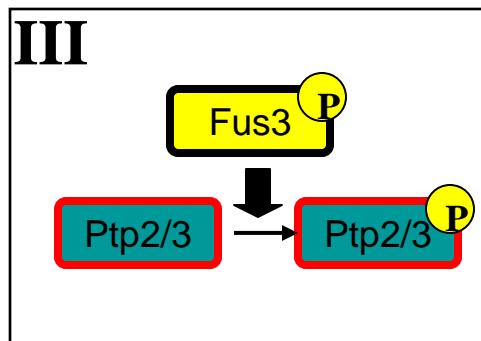
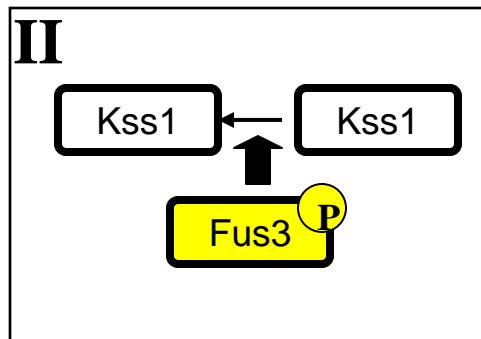
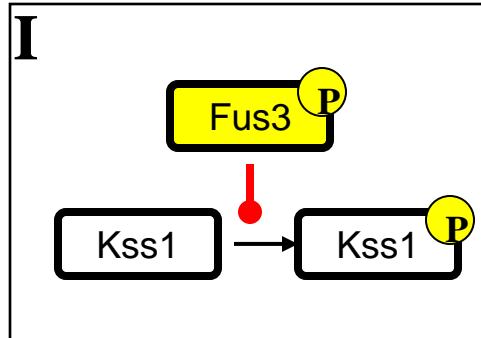


Evaluation of the Models



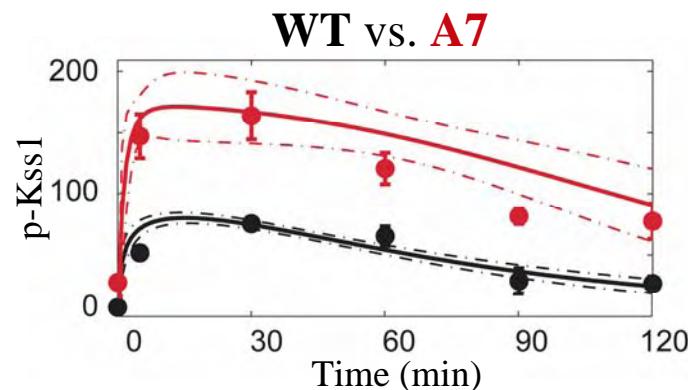
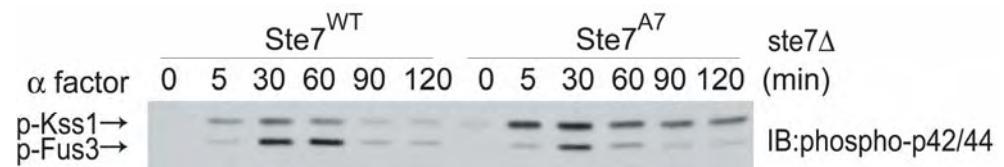
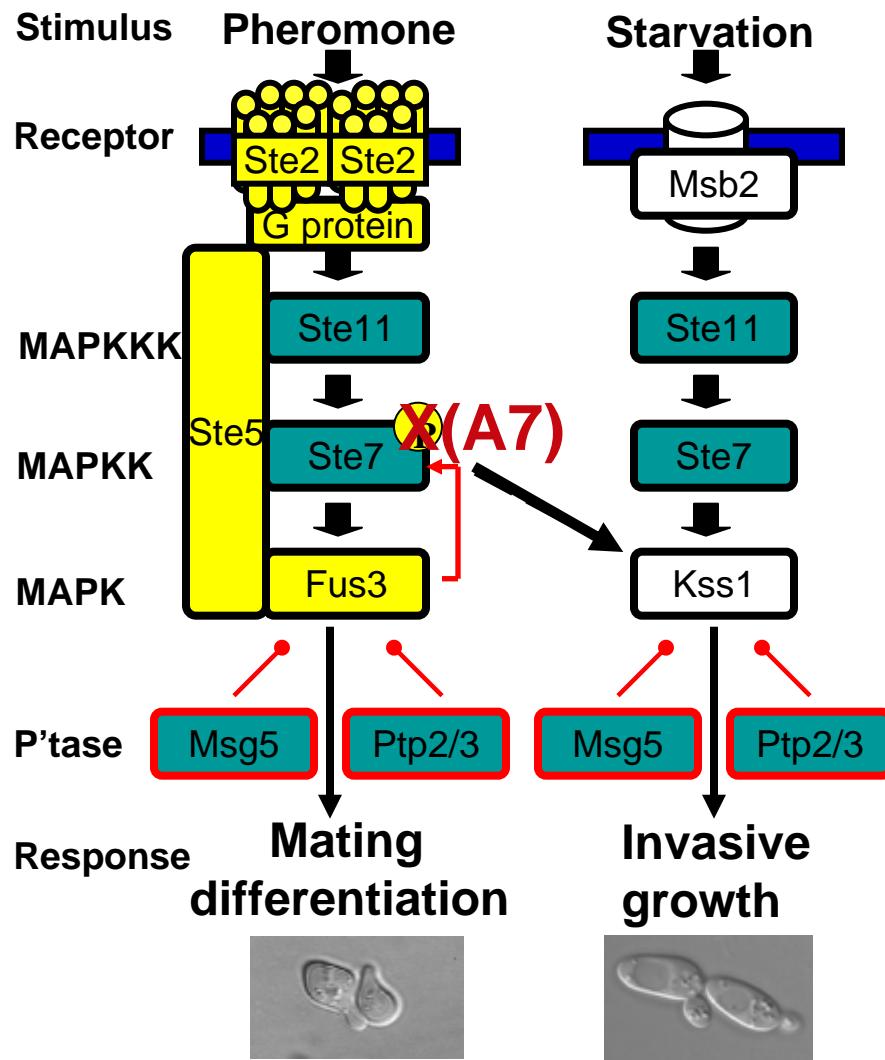


Comparison of the Models





Validation of the Model I





Conclusions

- A new mechanism of pathway specificity.
- Demonstrates utility of computational modeling in biology.



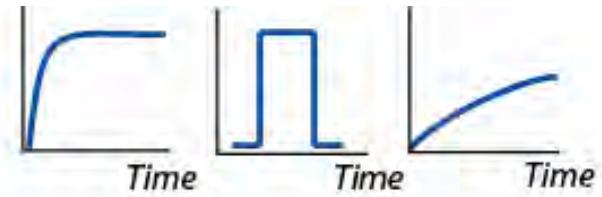
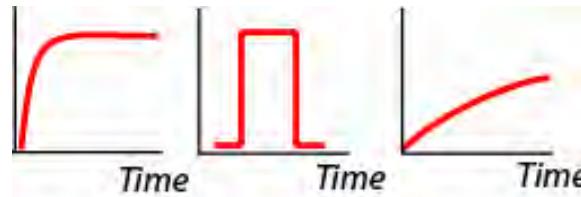
Outline

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- II. **Kinetic insulation as mechanism for signal specificity**



Signal Specificity

Signal



Receptor



Receptor

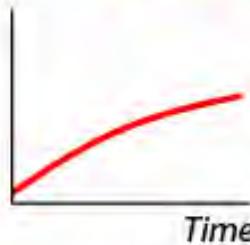


Common Component

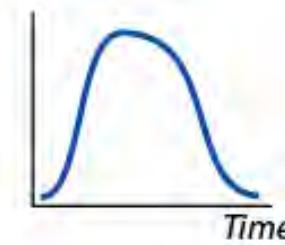
Terminal kinase



Response

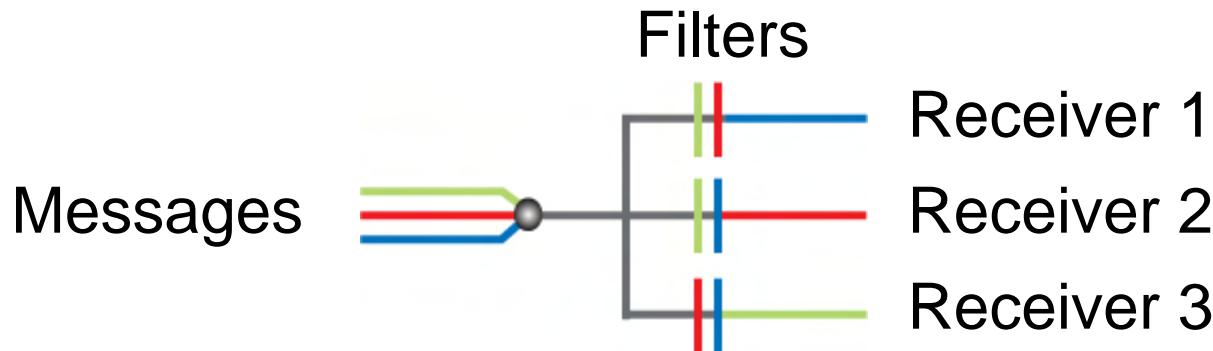


Terminal kinase

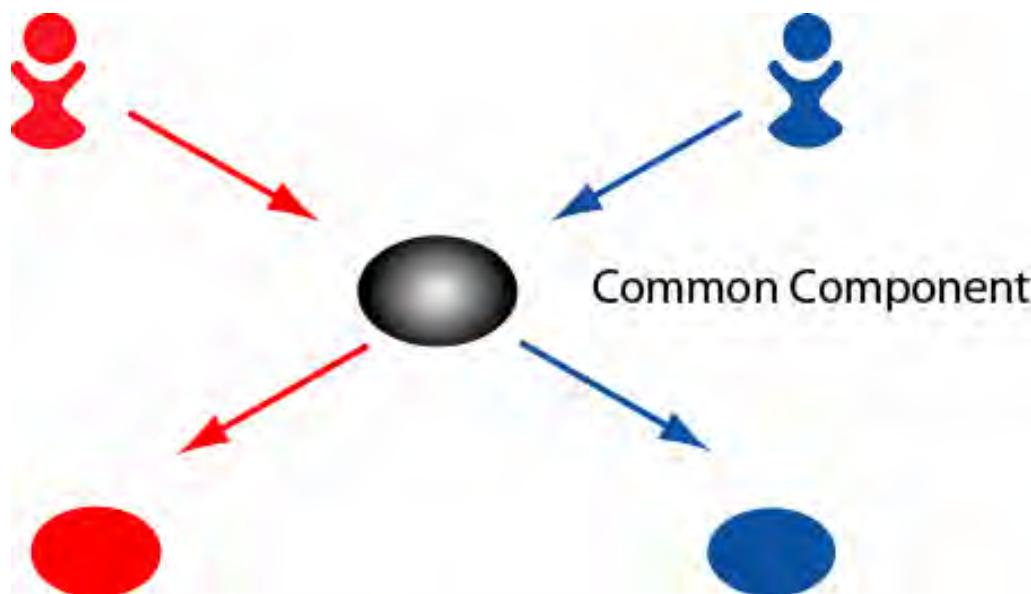




Information Transmission

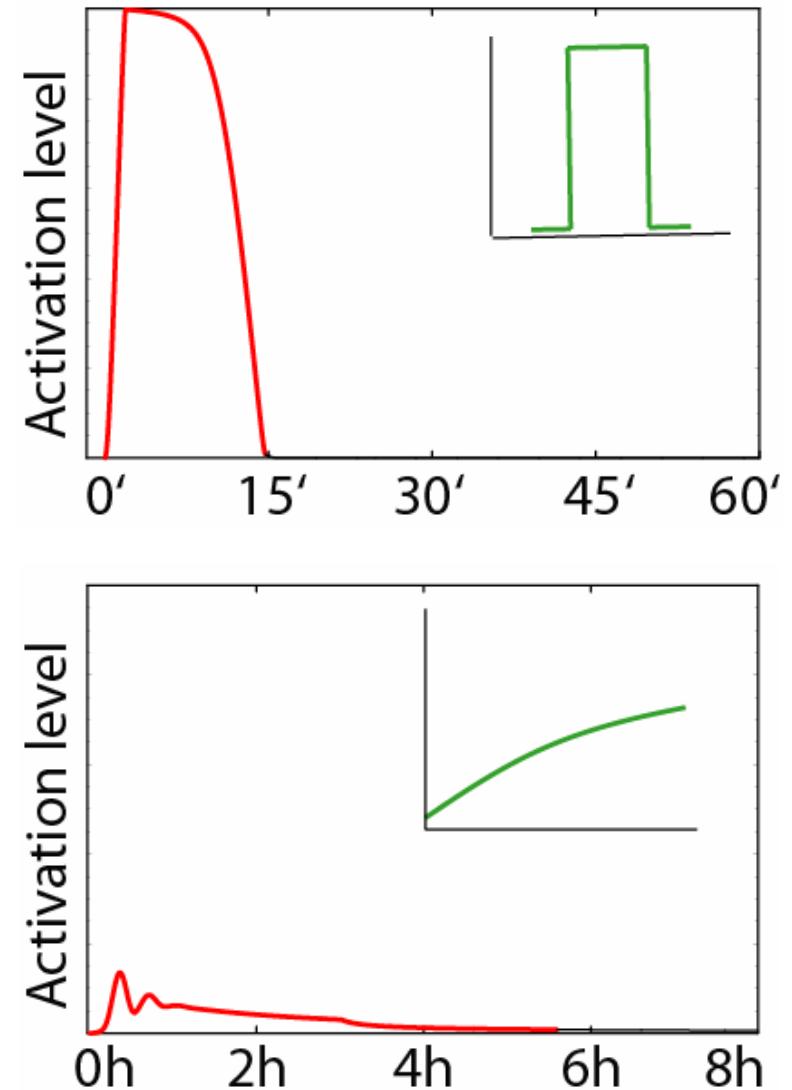
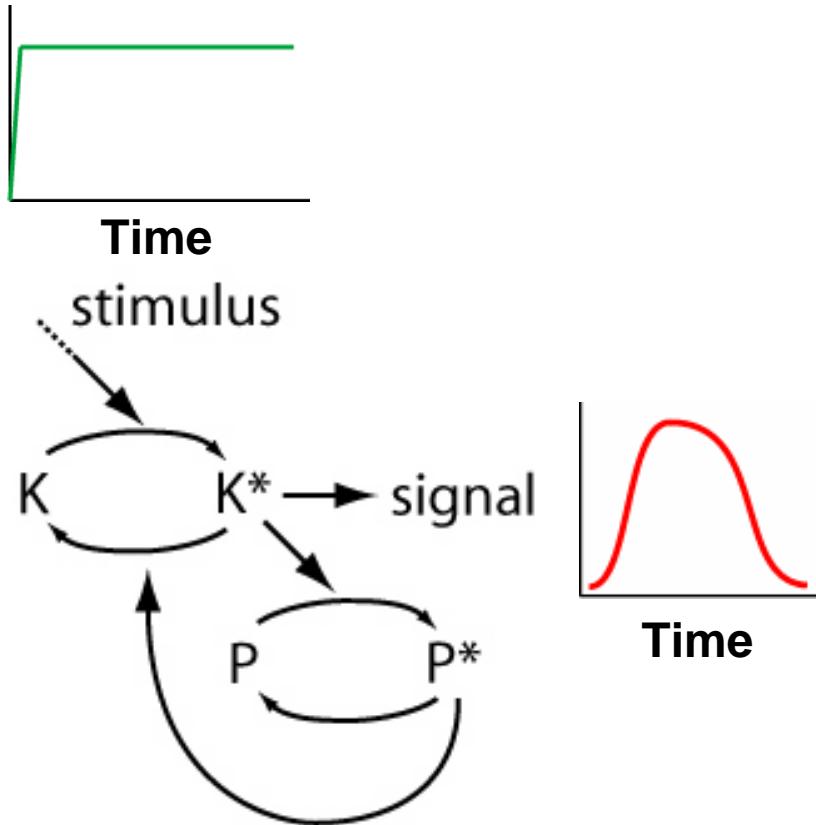


Can this approach be used in intracellular signaling networks?





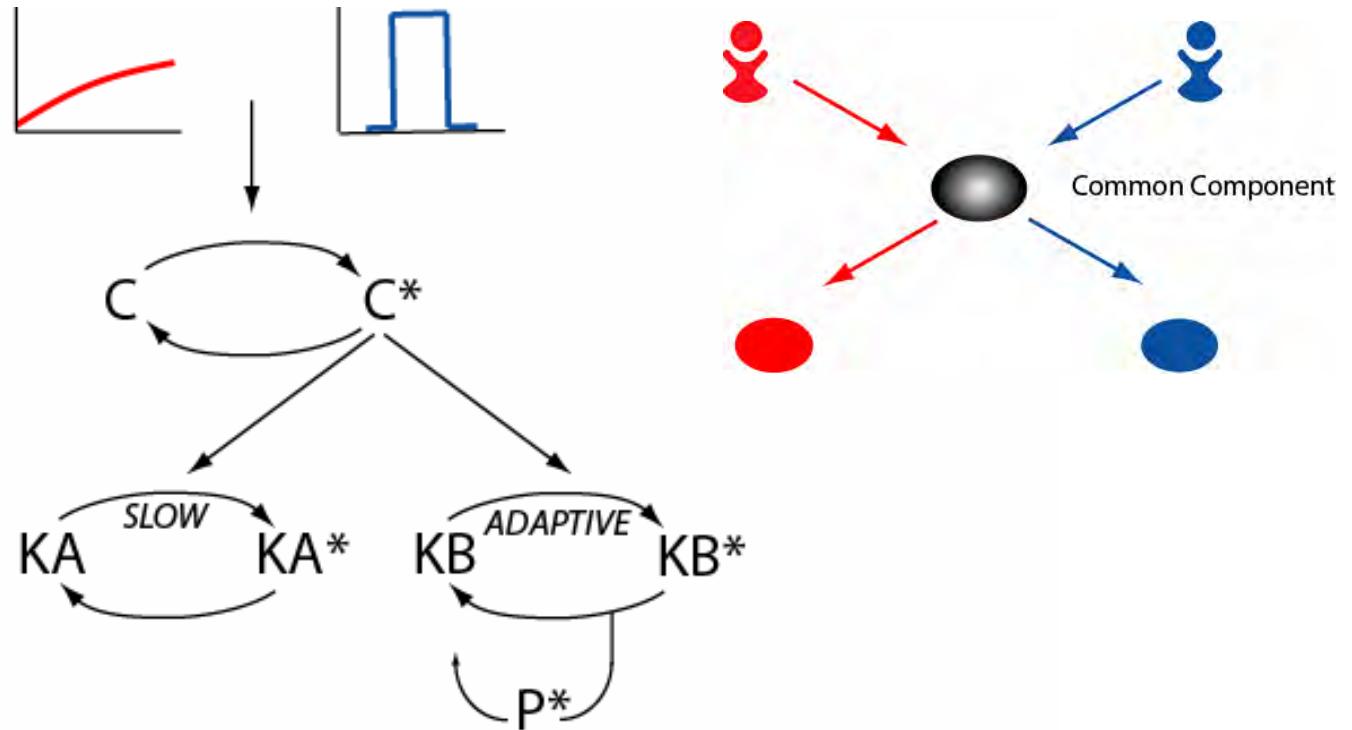
Adaptable systems act as a high pass filter





Downstream signal decoding

Input

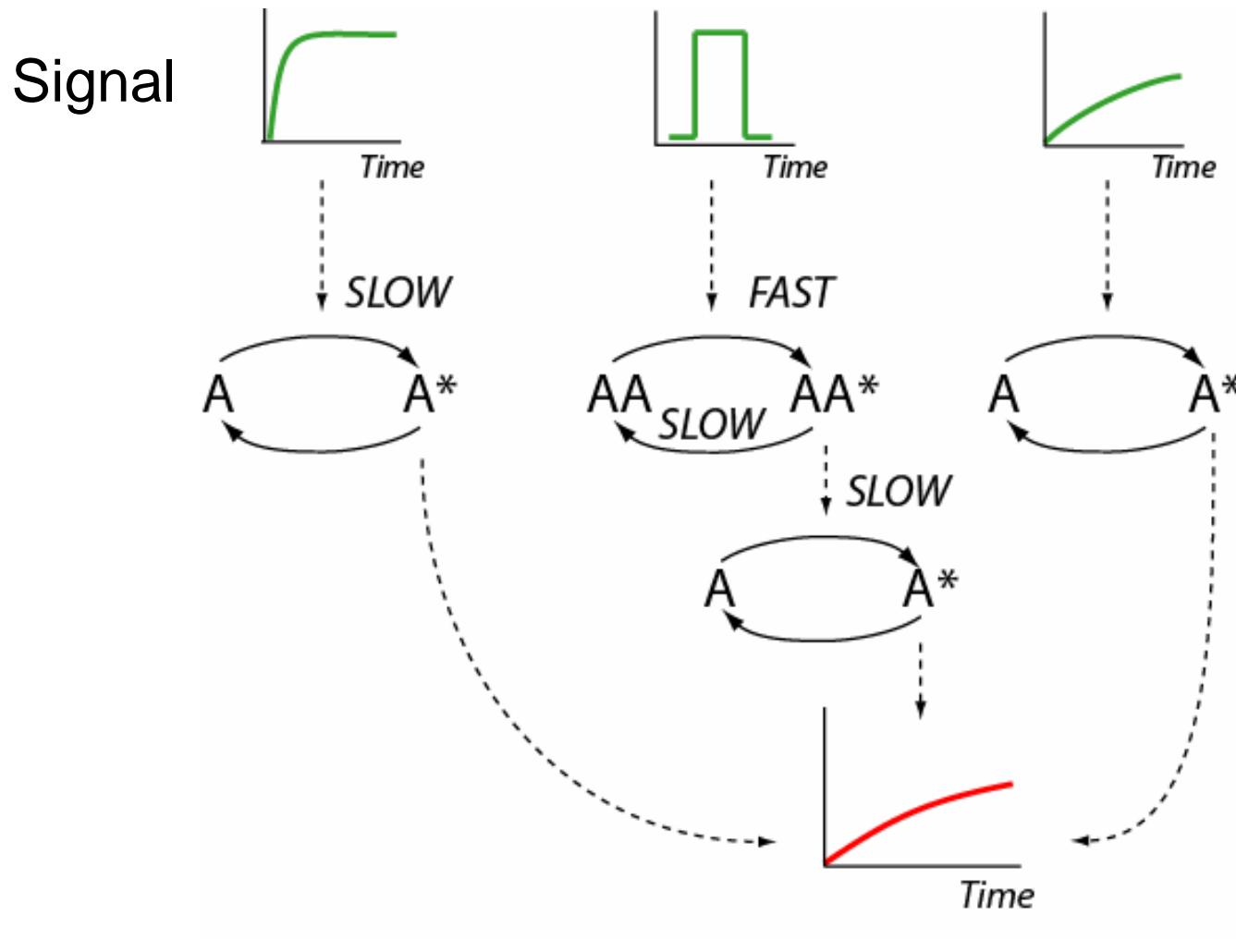


Response



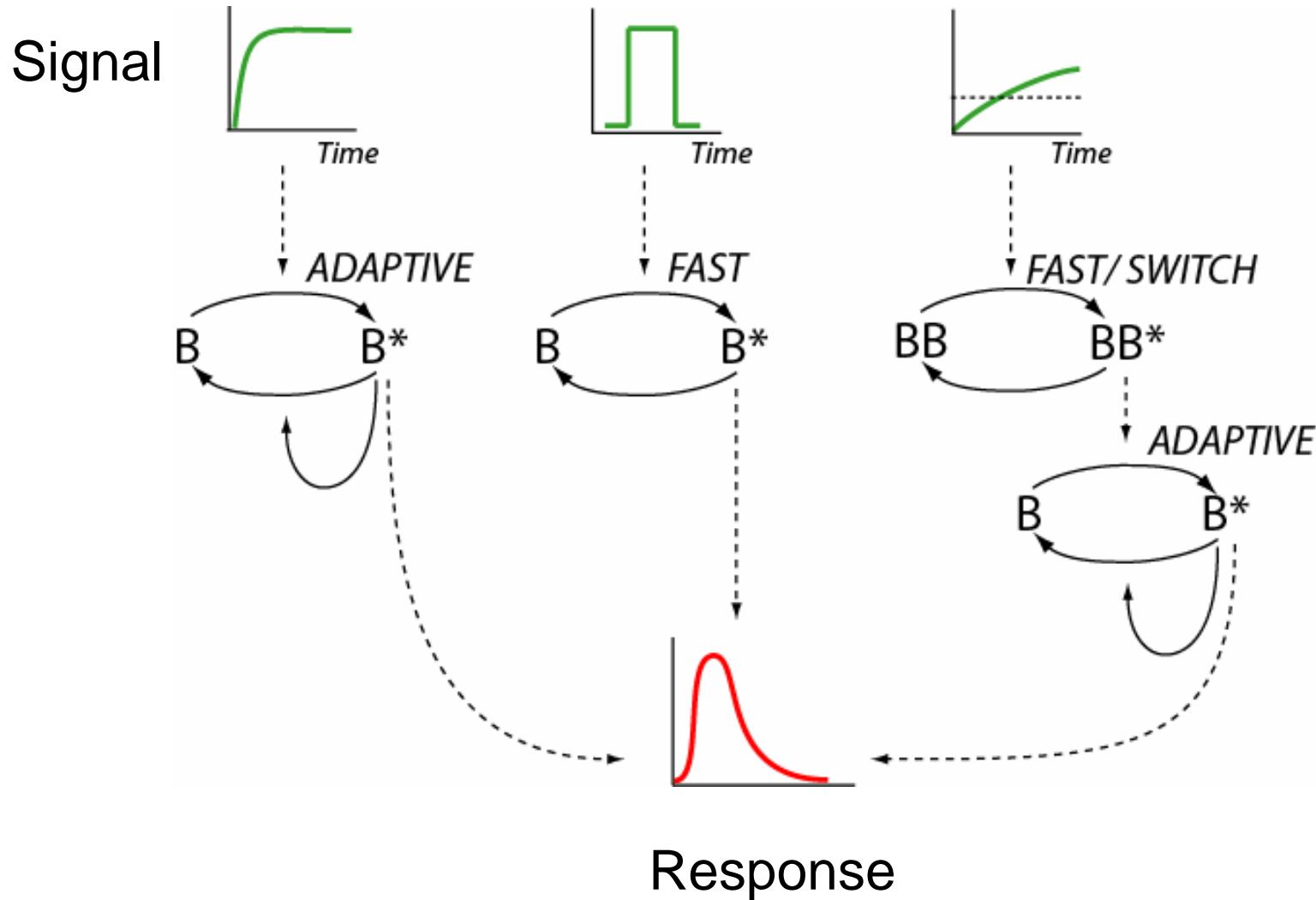


Upstream signal processing – slow response



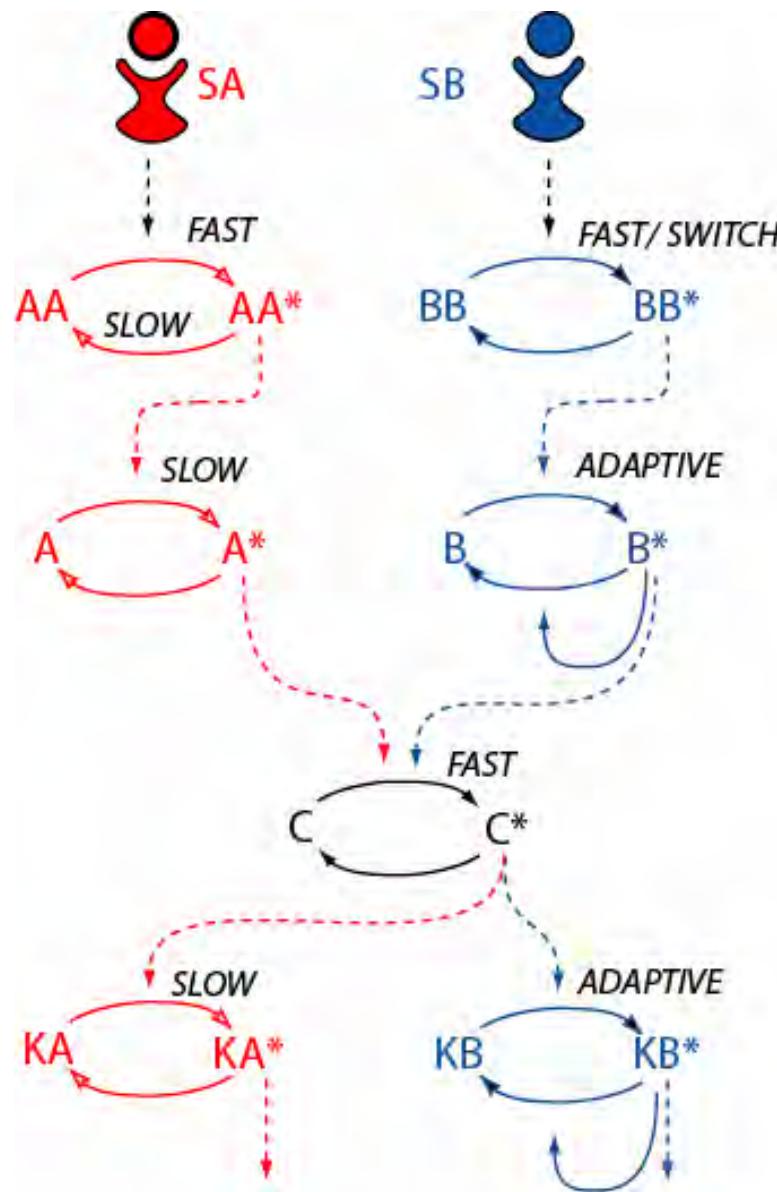


Transient response



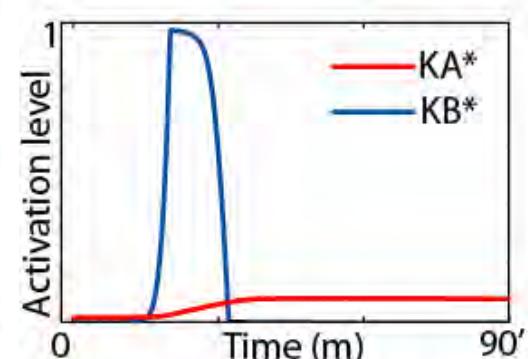
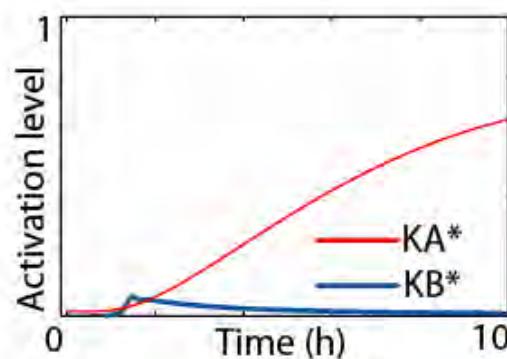
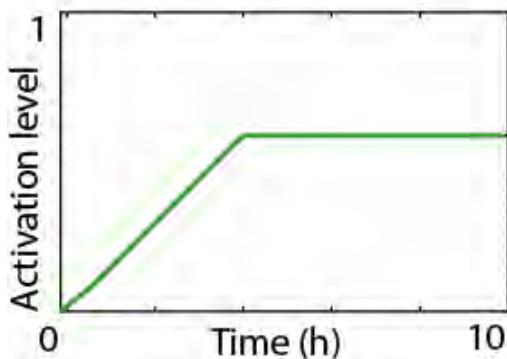
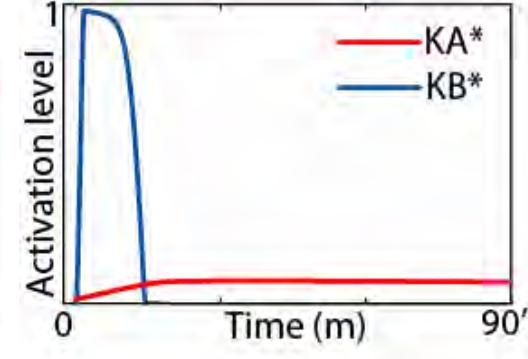
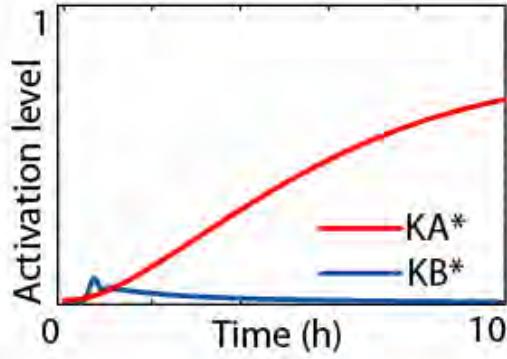
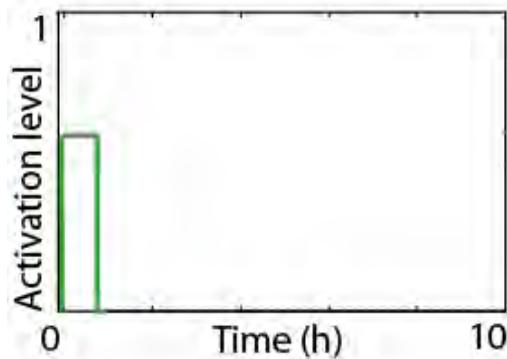
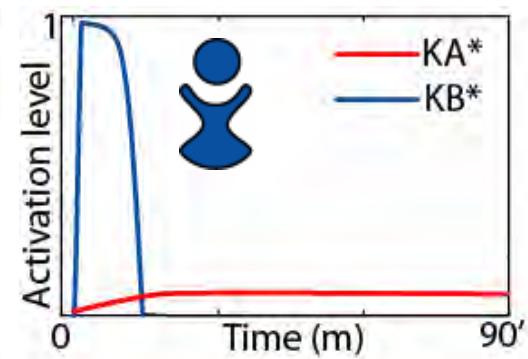
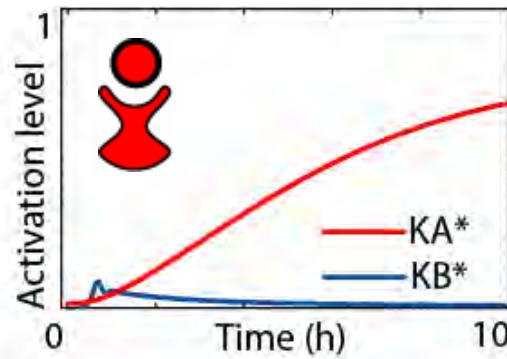
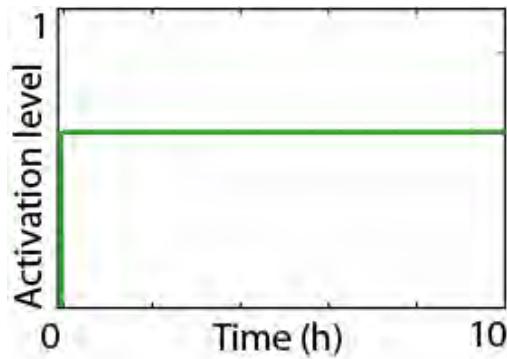


Specificity by kinetic insulation





Simulation results





Conclusions

- Kinetic insulation provides a potential mechanism of pathway specificity.
- Specificity is based solely on the temporal profile of the transmitted signal.
- Multilevel signaling cascades may have evolved to modulate the temporal profile of pathway activity.



Acknowledgements



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